IN THE SPECIFICATION:

Please amend the specification as follows:

Please replace the paragraph starting at page 50, line 6 and continuing through page 51, line 3 (paragraph [193]) with the following paragraph:

One example of an algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul et al., 1990. Software for performing BLAST analysis is publicly available through the world wide website of the National Center for Biotechnology Information ~~(http://www.ncbi.nlm.nih.gov/)~~. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold. See generally, Altschul et al., 1990. These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when the cumulative alignment score falls off by the quantity X from its maximum achieved value, the cumulative score goes to zero or below due to the accumulation of one or more negative scoring residue alignments, or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M = 5, N = 4, and a

comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix. See Henikoff & Henikoff, 1992.

Please replace the paragraph starting at page 75, line 17 and continuing through page 76, line 11 (paragraph [264]) with the following paragraph:

To further characterize the genes encoding the interacting proteins, the nucleic acid sequences of the baits and preys were compared with nucleic acid sequences present on Torrey Mesa Research Institute (TMRI)'s proprietary GENECHIP® Rice Genome Array (Affymetrix, Santa Clara, California, United States of America; see Zhu et al., 2001). The rice genome array contained 25-mer oligonucleotide probes with sequences corresponding to the 3' ends of 21,000 predicted open reading frames found in approximately 42,000 contigs that make up the rice genome map (see Goff et al., 2002). Sixteen different probes were used to measure the expression level of each nucleic acid. The sequences of the probes are available from the world wide website of the Torrey Mesa Research Institute (TMRI) ~~at http://tmri.org/gene_exp_web/~~. The calculated expression value was determined based on the observed expression level minus the noise background associated with each probe. Experiments included evaluating the differential gene expression from various plant tissues comprising seed, root, leaf and stem, panicle, and pollen. Gene expression was also measured in plants exposed to environmental cold (i.e., 14°C), osmotic pressure (growth media supplemented with 260 mM mannitol), drought (media supplemented with 25% polyethylene glycol 8000), salt (media supplemented with 150 mM NaCl), abscisic acid (ABA)-inducible stresses (media supplemented with 50 uM ABA; see Chen et al., 2002), infection by the fungal pathogen *Magnaporthe grisea*, and treatment with plant hormones (jasmonic acid (JA; 100 μM), gibberellin (GA3; 50 μM), and abscisic acid) and with herbicides benzylamino purine (BAP; 10 μM), 2,4-dichlorophenoxyacetic acid (2,4-D;2 mg/l ), and BL2 (10 μM)).